



7

SEQUENCE LISTING

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<120> Cloning of a Novel Inhibitor of Antigen-receptor Signalling by a Retroviral-based Functional Screen

<130> A-70219-1/RMS/DHR

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<150> US 60/260,953

<151> 2001-01-10

<160> 3

<170> PatentIn version 3.1

<210> 1

<211> 786

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(786)

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agt tcc tct gtc caa ggc cag gga cct gtg acc atg gaa gca gag aga	96
Ser Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg	
20 25 30	
agc aag gcc aca gcc gtg gcc ctg ggc agt ttc ccg gca ggt ggc ccg	144
Ser Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro	
35 40 45	
gcc gag ctg tcg ctg aga ctc ggg gag cca ttg acc atc gtc tct gag	192
Ala Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu	
50 55 60	

gat gga gac tgg tgg acg gtg ctg tct gaa gtc tca ggc aga gag tat Asp Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr 65 70 75 80	240
aac atc ccc agc gtc cac gtg gcc aaa gtc tcc cat ggg tgg ctg tat Asn Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr 85 90 95	288
gag ggc ctg agc agg gag aaa gca gag gaa ctg ctg ttg tta cct ggg Glu Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Leu Pro Gly 100 105 110	336
aac cct gga ggg gcc ttc ctc atc cgg gag agc cag acc agg aga ggc Asn Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly 115 120 125	384
tct tac tct ctg tca gtc cgc ctc agc cgc cct gca tcc tgg gac cgg Ser Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg 130 135 140	432
atc aga cac tac agg atc cac tgc ctt gac aat ggc tgg ctg tac atc Ile Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile 145 150 155 160	480
tca ccg cgc ctc acc ttc ccc tca ctc cag gcc ctg gtg gac cat tac Ser Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Val Asp His Tyr 165 170 175	528
tct gag ctg gcg gat gac atc tgc tgc cta ctc aag gag ccc tgt gtc Ser Glu Leu Ala Asp Asp Ile Cys Cys Leu Leu Lys Glu Pro Cys Val 180 185 190	576
ctg cag agg gct ggc ccg ctc cct ggc aag gat ata ccc cta cct gtg Leu Gln Arg Ala Gly Pro Leu Pro Gly Lys Asp Ile Pro Leu Pro Val 195 200 205	624
act gtg cag agg aca cca ctc aac tgg aaa gag ctg gac agc tcc ctc Thr Val Gln Arg Thr Pro Leu Asn Trp Lys Glu Leu Asp Ser Ser Leu 210 215 220	672
ctg ttt tct gaa gct gcc aca ggg gag gag tct ctt ctc agt gag ggt Leu Phe Ser Glu Ala Ala Thr Gly Glu Glu Ser Leu Leu Ser Glu Gly 225 230 235 240	720
ctc cgg gag tcc ctc agc ttc tac atc agc ctg aat gac gag gct gtc Leu Arg Glu Ser Leu Ser Phe Tyr Ile Ser Leu Asn Asp Glu Ala Val 245 250 255	768
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<212> PRT	

<213> Homo sapiens

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Met Gly Ser Leu Pro Ser Arg Arg Lys Ser Leu Pro Ser Pro Ser Leu
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Ser Ser Ser Val Gln Gly Gln Gly Pro Val Thr Met Glu Ala Glu Arg
20 25 30

Ser Lys Ala Thr Ala Val Ala Leu Gly Ser Phe Pro Ala Gly Gly Pro
35 40 45

Ala Glu Leu Ser Leu Arg Leu Gly Glu Pro Leu Thr Ile Val Ser Glu
50 55 60

Asp Gly Asp Trp Trp Thr Val Leu Ser Glu Val Ser Gly Arg Glu Tyr
65 70 75 80

Asn Ile Pro Ser Val His Val Ala Lys Val Ser His Gly Trp Leu Tyr
85 90 95

Glu Gly Leu Ser Arg Glu Lys Ala Glu Glu Leu Leu Leu Leu Pro Gly
100 105 110

Asn Pro Gly Gly Ala Phe Leu Ile Arg Glu Ser Gln Thr Arg Arg Gly
115 120 125

Ser Tyr Ser Leu Ser Val Arg Leu Ser Arg Pro Ala Ser Trp Asp Arg
130 135 140

Ile Arg His Tyr Arg Ile His Cys Leu Asp Asn Gly Trp Leu Tyr Ile
145 150 155 160

Ser Pro Arg Leu Thr Phe Pro Ser Leu Gln Ala Leu Val Asp His Tyr
165 170 175

Ser Glu Leu Ala Asp Asp Ile Cys Cys Leu Leu Lys Glu Pro Cys Val
180 185 190

Leu Gln Arg Ala Gly Pro Leu Pro Gly Lys Asp Ile Pro Leu Pro Val
195 200 205

Thr Val Gln Arg Thr Pro Leu Asn Trp Lys Glu Leu Asp Ser Ser Leu

210

215

220

Leu Phe Ser Glu Ala Ala Thr Gly Glu Glu Ser Leu Leu Ser Glu Gly
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Leu Arg Glu Ser Leu Ser Phe Tyr Ile Ser Leu Asn Asp Glu Ala Val
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Ser Leu Asp Asp Ala
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 <213> Homo sapiens

<400> 3

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 20 25 30

Tyr Pro Ser Pro Asp Ile Ser Pro Pro Ile Phe Arg Arg Gly Glu Lys
 35 40 45

Leu Arg Val Ile Ser Asp Glu Gly Gly Trp Trp Lys Ala Ile Ser Leu
 50 55 60

Ser Thr Gly Arg Glu Ser Tyr Ile Pro Gly Ile Cys Val Ala Arg Val
 65 70 75 80

Tyr His Gly Trp Leu Phe Glu Gly Leu Gly Arg Asp Lys Ala Glu Glu
 85 90 95

Leu Leu Gln Leu Pro Asp Thr Lys Val Gly Ser Phe Met Ile Arg Glu
 100 105 110

Ser Glu Thr Lys Lys Gly Phe Tyr Ser Leu Ser Val Arg His Arg Gln
 115 120 125

Val Lys His Tyr Arg Ile Phe Arg Leu Pro Asn Asn Trp Tyr Tyr Ile
 130 135 140

Ser Pro Arg Leu Thr Phe Gln Cys Leu Glu Asp Leu Val Asn His Tyr
 145 150 155 160

Ser Glu Val Ala Asp Gly Leu Cys Cys Val Leu Thr Thr Pro Cys Leu
 165 170 175

Thr Gln Ser Thr Ala Ala Pro Ala Val Arg Ala Ser Ser Ser Pro Val
 180 185 190

Thr Leu Arg Gln Lys Thr Val Asp Trp Arg Arg Val Ser Arg Leu Gln
 195 200 205

Glu Asp Pro Glu Gly Thr Glu Asn Pro Leu Gly Val Asp Glu Ser Leu
 210 215 220

Phe Ser Tyr Gly Leu Arg Glu Ser Ile Ala Ser Tyr Leu Ser Leu Thr
 225 230 235 240

Ser Glu Asp Asn Thr Ser Phe Asp Arg Lys Lys Lys Ser Ile Ser Leu
 245 250 255

Met Tyr Gly Gly Ser Lys Arg Lys Ser Ser Phe Phe Ser Ser Pro Pro
 260 265 270

Tyr Phe Glu Asp
 275